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 GTTCAGTCTA TGTTTGCTCC AACTGACACT TCAGATATGG AAGCAGTATG 550
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 TCTGAGTTCT TCTTTGGATG ACACCGAAGT TAAGAAGGTT ATGGAAGAAT 750
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 AAGATTGCCT TGTAGAGGTA GCATGCACAG GATGGTAAAT TGGATTGGTG 1000
 GATCCACCAT ATCATGGGAT TTAAATTTAT CATAACCATG TGTA AAAAGA 1050
 AATTAATGTA TGATGACATC TCACAGGTCT TGCCTTTAAA TTACCCCTCC 1100
 CTGCACACAC ATACACAGAT ACACACACAC AAATATAATG TAACGATCTT 1150
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 CTTTATTAAT GACAAGGGAA ACCATGAGTA ATGCCACAAT GGCATATTGT 1250
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<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

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				20					25					30
Lys	Leu	Gly	Asn	Pro	Thr	Asp	Arg	Asn	Val	Cys	Phe	Lys	Val	Lys
				35					40					45
Thr	Thr	Ala	Pro	Arg	Arg	Tyr	Cys	Val	Arg	Pro	Asn	Ser	Gly	Ile
				50					55					60
Ile	Asp	Ala	Gly	Ala	Ser	Ile	Asn	Val	Ser	Val	Met	Leu	Gln	Pro
				65					70					75
Phe	Asp	Tyr	Asp	Pro	Asn	Glu	Lys	Ser	Lys	His	Lys	Phe	Met	Val
				80					85					90
Gln	Ser	Met	Phe	Ala	Pro	Thr	Asp	Thr	Ser	Asp	Met	Glu	Ala	Val
				95					100					105
Trp	Lys	Glu	Ala	Lys	Pro	Glu	Asp	Leu	Met	Asp	Ser	Lys	Leu	Arg
				110					115					120
Cys	Val	Phe	Glu	Leu	Pro	Ala	Glu	Asn	Asp	Lys	Pro	His	Asp	Val
				125					130					135
Glu	Ile	Asn	Lys	Ile	Ile	Ser	Thr	Thr	Ala	Ser	Lys	Thr	Glu	Thr
				140					145					150

Pro	Ile	Val	Ser	Lys	Ser	Leu	Ser	Ser	Ser	Leu	Asp	Asp	Thr	Glu
				155					160					165
Val	Lys	Lys	Val	Met	Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Val
				170					175					180
Gln	Arg	Leu	Arg	Glu	Glu	Asn	Lys	Gln	Phe	Lys	Glu	Glu	Asp	Gly
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Leu	Arg	Met	Arg	Lys	Thr	Val	Gln	Ser	Asn	Ser	Pro	Ile	Ser	Ala
				200					205					210
Leu	Ala	Pro	Thr	Gly	Lys	Glu	Glu	Gly	Leu	Ser	Thr	Arg	Leu	Leu
				215					220					225
Ala	Leu	Val	Val	Leu	Phe	Phe	Ile	Val	Gly	Val	Ile	Ile	Gly	Lys
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Ile Ala Leu

<210> 285
 <211> 418
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 40, 53, 68, 119, 134, 177-178, 255
 <223> unknown base

<400> 285
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 cagcagtttt ggggtggggag caagggnga gagaaactct tcagcgaatc 200
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 taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
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<210> 286
 <211> 543
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 73, 97